

SEQUENCE LISTING

<110> Franciso, Joseph
McDonagh, Charlotte

<120> MODIFIED L49-sFv EXHIBITING INCREASED STABILITY AND METHODS OF USE
THEREOF

<130> 9632-082-999

<140> 10/537,143 (National stage of PCT/US02/38414)

<141> 2002-12-02 (371c date)

<160> 23

<170> PatentIn version 3.0

<210> 1

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(753)

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Gln Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser	
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ggg tac tgg aac tgg atc cgg aag ttc cca ggg aat aaa ctt gaa tat	144
Gly Tyr Trp Asn Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Glu Tyr	
35 40 45	
atg ggt tac ata agc gac agt ggt atc act tac tac aat cca tct ctc	192
Met Gly Tyr Ile Ser Asp Ser Gly Ile Thr Tyr Tyr Asn Pro Ser Leu	
50 55 60	
aaa agt cgc att tcc atc act cga gac aca tcc aag aac caa tac tac	240
Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Tyr	
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ctc cag ttg aat ttt gtg act gct gag gac aca gcc aca tat aac tgt	288
Leu Gln Leu Asn Phe Val Thr Ala Glu Asp Thr Ala Thr Tyr Asn Cys	
85 90 95	
gca aga agg act ctg gct act tac tat gct atg gac tac tgg ggt caa	336
Ala Arg Arg Thr Leu Ala Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln	
100 105 110	
gga acc tct gtc acc gtc tcc tca ggc tcg acg tcc ggc tct ggc aaa	384
Gly Thr Ser Val Thr Val Ser Ser Gly Ser Thr Ser Gly Ser Gly Lys	
115 120 125	
ccg ggc tct ggc gaa ggc tot acc aag ggc gat ttt gtg atg acc caa	432
Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Asp Phe Val Met Thr Gln	
130 135 140	
act cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct	480
Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser	
145 150 155 160	
tgc agg gct agt cag agc ctt gta cac agt aat gga aac acc tat tta	528
Cys Arg Ala Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu	
165 170 175	
cat tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac	576

His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr		
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Arg	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser		
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Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu		
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ttc	ggt	gga	ggc	acc	aag	ctg	gaa	atc	aaa	cgg						753	
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<212> DNA
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<220>
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<222> (1)..(1839)

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cag act ctg tcc ctc acc tgt tct gtc act ggc gac tcc atc acc agt	96
Gln Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser	
20 25 30	
ggg tac tgg aac tgg atc cgg aag ttc cca ggg aat aaa ctt gaa tat	144
Gly Tyr Trp Asn Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Glu Tyr	
35 40 45	
atg ggt tac ata agc gac agt ggt atc act tac tac aat cca tct ctc	192
Met Gly Tyr Ile Ser Asp Ser Gly Ile Thr Tyr Tyr Asn Pro Ser Leu	
50 55 60	
aaa agt cgc att tcc atc act cga gac aca tcc aag aac caa tac tac	240
Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Tyr	
65 70 75 80	
ctc cag ttg aat ttt gtg act gct gag gac aca gcc aca tat aac tgt	288
Leu Gln Leu Asn Phe Val Thr Ala Glu Asp Thr Ala Thr Tyr Asn Cys	
85 90 95	
gca aga agg act ctg gct act tac tat gct atg gac tac tgg ggt caa	336
Ala Arg Arg Thr Leu Ala Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln	
100 105 110	
gga acc tct gtc acc gtc tcc tca ggc tcg acg tcc ggc tct ggc aaa	384
Gly Thr Ser Val Thr Val Ser Ser Gly Ser Thr Ser Gly Ser Gly Lys	
115 120 125	
ccg ggc tct ggc gaa ggc tct acc aag ggc gat ttt gtg atg acc caa	432
Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Asp Phe Val Met Thr Gln	
130 135 140	
act cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct	480
Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser	
145 150 155 160	
tgc agg gct agt cag agc ctt gta cac agt aat gga aac acc tat tta	528
Cys Arg Ala Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu	
165 170 175	
cat tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac	576
His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Ile Tyr	
180 185 190	
aga gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt	624
Arg Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser	
195 200 205	
gga tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag	672
Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu	
210 215 220	
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Lys	Gln	Leu	Ala	Glu	Val	Val	Ala	Asn	Thr	Ile	Thr	Pro	Leu	Met	Lys	
			260					265					270			
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Ala	Gln	Ser	Val	Pro	Gly	Met	Ala	Val	Ala	Val	Ile	Tyr	Gln	Gly	Lys	
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Pro	His	Tyr	Tyr	Thr	Phe	Gly	Lys	Ala	Asp	Ile	Ala	Ala	Asn	Lys	Pro	
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Thr	Gly	Val	Leu	Gly	Gly	Asp	Ala	Ile	Ala	Arg	Gly	Glu	Ile	Ser	Leu	
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Phe	Tyr	Gln	Asn	Trp	Gln	Pro	Gln	Trp	Lys	Pro	Gly	Thr	Thr	Arg	Leu	
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Tyr	Ala	Asn	Ala	Ser	Ile	Gly	Leu	Phe	Gly	Ala	Leu	Ala	Val	Lys	Pro	
				405				410						415		
tct	ggc	atg	ccc	tat	gag	cag	gcc	atg	acg	acg	cgg	gtc	ctt	aag	ccg	1296
Ser	Gly	Met	Pro	Tyr	Glu	Gln	Ala	Met	Thr	Thr	Arg	Val	Leu	Lys	Pro	
			420					425					430			
ctc	aag	ctg	gac	cat	acc	tgg	att	aac	gtg	ccg	aaa	gcg	gaa	gag	gcg	1344
Leu	Lys	Leu	Asp	His	Thr	Trp	Ile	Asn	Val	Pro	Lys	Ala	Glu	Glu	Ala	
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His	Tyr	Ala	Trp	Gly	Tyr	Arg	Asp	Gly	Lys	Ala	Val	Arg	Val	Ser	Pro	
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ggt	atg	ctg	gat	gca	caa	gcc	tat	ggc	gtg	aaa	acc	aac	gtg	cag	gat	1440
Gly	Met	Leu	Asp	Ala	Gln	Ala	Tyr	Gly	Val	Lys	Thr	Asn	Val	Gln	Asp	
465				470						475					480	
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Met	Ala	Asn	Trp	Val	Met	Ala	Asn	Met	Ala	Pro	Glu	Asn	Val	Ala	Asp	
				485				490						495		
gcc	tca	ctt	aag	cag	ggc	atc	gcg	ctg	gcg	cag	tcg	cgc	tac	tgg	cgt	1536
Ala	Ser	Leu	Lys	Gln	Gly	Ile	Ala	Leu	Ala	Gln	Ser	Arg	Tyr	Trp	Arg	
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Ile	Gly	Ser	Met	Tyr	Gln	Gly	Leu	Gly	Trp	Glu	Met	Leu	Asn	Trp	Pro	
			515				520					525				
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Val	Glu	Ala	Asn	Thr	Val	Val	Glu	Thr	Ser	Phe	Gly	Asn	Val	Ala	Leu	
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Ala Ser Trp Val His	Lys Thr Gly Ser Thr	Gly Gly Phe Gly Ser Tyr					
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gtg gcc ttt att cct	gaa aag cag atc ggt	att gtg atg ctc gcg aat	1776				
Val Ala Phe Ile Pro	Glu Lys Gln Ile Gly	Ile Val Met Leu Ala Asn					
	580	585	590				
aca agc tat ccg aac	ccg gca cgc gtt gag	gcg gca tac cat atc ctc	1824				
Thr Ser Tyr Pro Asn	Pro Ala Arg Val Glu	Ala Ala Tyr His Ile Leu					
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gag gcg cta cag tag			1839				
Glu Ala Leu Gln							
610							

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 35 40 45
 Met Gly Tyr Ile Ser Asp Ser Gly Ile Thr Tyr Tyr Asn Pro Ser Leu
 50 55 60
 Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Tyr
 65 70 75 80
 Leu Gln Leu Asn Phe Val Thr Ala Glu Asp Thr Ala Thr Tyr Asn Cys
 85 90 95
 Ala Arg Arg Thr Leu Ala Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Ser Val Thr Val Ser Ser Gly Ser Thr Ser Gly Ser Gly Lys
 115 120 125
 Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Asp Phe Val Met Thr Gln
 130 135 140
 Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser
 145 150 155 160
 Cys Arg Ala Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu
 165 170 175
 His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
 180 185 190
 Arg Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
 195 200 205
 Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu
 210 215 220

Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Pro	Thr	225	230	235	240
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Thr	Pro	Val	Ser	Glu	245	250	255	
Lys	Gln	Leu	Ala	Glu	Val	Val	Ala	Asn	Thr	Ile	Thr	Pro	Leu	Met	Lys	260	265	270	
Ala	Gln	Ser	Val	Pro	Gly	Met	Ala	Val	Ala	Val	Ile	Tyr	Gln	Gly	Lys	275	280	285	
Pro	His	Tyr	Tyr	Thr	Phe	Gly	Lys	Ala	Asp	Ile	Ala	Ala	Asn	Lys	Pro	290	295	300	
Val	Thr	Pro	Gln	Thr	Leu	Phe	Glu	Leu	Gly	Ser	Ile	Ser	Lys	Thr	Phe	305	310	315	320
Thr	Gly	Val	Leu	Gly	Gly	Asp	Ala	Ile	Ala	Arg	Gly	Glu	Ile	Ser	Leu	325	330	335	
Asp	Asp	Ala	Val	Thr	Arg	Tyr	Trp	Pro	Gln	Leu	Thr	Gly	Lys	Gln	Trp	340	345	350	
Gln	Gly	Ile	Arg	Met	Leu	Asp	Leu	Ala	Thr	Tyr	Thr	Ala	Gly	Gly	Leu	355	360	365	
Pro	Leu	Gln	Val	Pro	Asp	Glu	Val	Thr	Asp	Asn	Ala	Ser	Leu	Leu	Arg	370	375	380	
Phe	Tyr	Gln	Asn	Trp	Gln	Pro	Gln	Trp	Lys	Pro	Gly	Thr	Thr	Arg	Leu	385	390	395	400
Tyr	Ala	Asn	Ala	Ser	Ile	Gly	Leu	Phe	Gly	Ala	Leu	Ala	Val	Lys	Pro	405	410	415	
Ser	Gly	Met	Pro	Tyr	Glu	Gln	Ala	Met	Thr	Thr	Arg	Val	Leu	Lys	Pro	420	425	430	
Leu	Lys	Leu	Asp	His	Thr	Trp	Ile	Asn	Val	Pro	Lys	Ala	Glu	Glu	Ala	435	440	445	
His	Tyr	Ala	Trp	Gly	Tyr	Arg	Asp	Gly	Lys	Ala	Val	Arg	Val	Ser	Pro	450	455	460	
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Met	Ala	Asn	Trp	Val	Met	Ala	Asn	Met	Ala	Pro	Glu	Asn	Val	Ala	Asp	485	490	495	
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Ile	Gly	Ser	Met	Tyr	Gln	Gly	Leu	Gly	Trp	Glu	Met	Leu	Asn	Trp	Pro	515	520	525	
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Ala Pro Leu Pro Val Ala Glu Val Asn Pro Pro Ala Pro Pro Val Lys
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Ala Ser Trp Val His Lys Thr Gly Ser Thr Gly Gly Phe Gly Ser Tyr
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Val Ala Phe Ile Pro Glu Lys Gln Ile Gly Ile Val Met Leu Ala Asn
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Thr Ser Tyr Pro Asn Pro Ala Arg Val Glu Ala Ala Tyr His Ile Leu
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<210> 6
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<400> 19
 acagccacat attactgtgc aagaagg 27

<210> 20
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<213> Artificial

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<223> Description of Artificial Sequence: Primer

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27

<210> 21

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<210> 22

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<212> DNA

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<212> PRT

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Met His Gly Thr Lys Leu

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